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Drosophila melanogaster BAC library, partial EcoRI in
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1159 catcacctgtgcagctctccacagag 1186
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db 54075 CATCACCTGTGCGAGTCTCTCAAGAG 54048

RESULT 6
LOCUS DROSETS4
DEFINITION Drosophila melanogaster D-ets-4 DNA binding domain protein gene, 3'
ACCESSION M88474
MID M88474.1 GI:157195
VERSION M88474.1 GI:157195
KEYWORDS DNA-binding domain protein.
SOURCE Drosophila melanogaster DNA.
ORGANISM Drosophila melanogaster;
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 362)
AUTHORS Chen,T., Buntling,M., Karim,F.D. and Thummel,C.S.
TITLE Isolation and characterization of five Drosophila genes that encode
an ets-related DNA binding domain
JOURNAL Dev Biol. 151, 176-191 (1992)
FEATURES
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ORIGIN Chromosome 3L 98B.

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Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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db 75 CATCACCTGTGCGAGTCTCTCAAGAG 102
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RESULT 7
LOCUS HSDNAFEV3
DEFINITION H. sapiens FEV gene, exon 3.
ACCESSION Y08979
MID Y08979.1 GI:1841699
VERSION Y08979.1 GI:1841699
KEYWORDS ets gene family.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 1403)
AUTHORS Peter,M., Couturier,J., Pacquemenet,H., Michon,J., Thomas,G.,
Magdelenat,H. and Delattre,O.
TITLE A new member of the ETS family fused to EWS in Ewing tumors
JOURNAL Oncogene 14 (10), 1159-1164 (1997)
MEDLINE 9723656
REFERENCE 2 (bases 1 to 1403)
AUTHORS Delattre,O.
KEYWORDS Ewing sarcoma
SOURCE Submitted (10-OCT-1995) O. Delattre, Institut Curie, Inserm U434,
26 Rue Pulin, Paris 75231 Cedex 05, Paris 75231 Cedex 05, FRANCE
REMARK 3 (bases 1 to 1403)
REFERENCE 3 (bases 1 to 1403)
AUTHORS Delattre,O.
TITLE Direct Submision
JOURNAL Submitted (13-FEB-1997) O. Delattre, Institut Curie, Inserm U434,
26 Rue Pulin, Paris 75231 Cedex 05, Paris 75231 Cedex 05, FRANCE
COMMENT On Feb 13, 1997, a new version replaced 91:1834485.
FEATURES
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/number=3
/evidence="experimental"
BASE COUNT 210 a 551 c 376 g 266 t
ORIGIN

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db 398 CATGACACACACACAGCTGACGCGC 422

RESULT 8
LOCUS HSRNAFEV
DEFINITION H. sapiens mRNA for FEV protein.
ACCESSION Y08976
MID Y08976.1 GI:1834508
VERSION Y08976.1 GI:1834508
KEYWORDS ets gene family.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Vertebrata; Mammalia; Eutheria;

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REFERENCE 1 Primates: Catarrhini: Homiidae: Homo.
 1 (bases 1 to 1901)
 AUTHORS Peter,M., Couturier,J., Pacquement,H., Michon,J., Thomas,G.,
 Magdelenat,H. and Delattre,O.
 TITLE A new member of the ETS family fused to BMS in Ewing tumors
 JOURNAL Oncogene 14 (10), 1159-1164 (1997)
 MEDLINE 97/24555
 REFERENCE 2 (bases 1 to 1901)
 AUTHORS Delattre,O.
 TITLE Direct Substitution
 JOURNAL Submitted (10-OCT-1996) O. Delattre, Institut Curie, Inserm U434,
 26 Rue Dum. Paris 75231 Cedex 05, Paris 75231 Cedex 05, FRANCE
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 Db 869 CATGACTGACGACACTGAGCCG 893
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 LOCUS DRODET56A 480 bp DNA INV
 DEFINITION Drosophila melanogaster D-ets-6 DNA binding domain protein gene,
 partial cds.
 ACCESSION AF057197
 MID M88475.1 GI:157197
 VERSION 88475.1
 KEYWORDS DNA-binding domain protein.
 SOURCE Drosophila melanogaster.
 ORGANISM Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Muscivora; Neoptera; Endopterygota; Diptera; Brachycera;
 1 (bases 1 to 480)
 AUTHORS Chen,T., Bunting,N., Karim,F.D. and Hummel,C.S.
 TITLE Isolation and characterization of five Drosophila genes that encode
 an ets-related DNA binding domain
 JOURNAL Dev. Biol. 151, 176-191 (1992)
 MEDLINE 92249640
 FEATURES
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 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1312 catgaactcagcaacgctgagccg 1335
 Db 256 CATGACTGACGACACTGAGCCG 279
 RESULT 10
 LOCUS AC004573/C 85095 bp DNA INV
 DEFINITION Drosophila melanogaster. Chromosome 2L, region 21C5-21D1, P1 clone
 AC004573 complete sequence.
 ACCESSION AC004573
 MID 94204255
 VERSION AC004573.1 GI:4204255
 KEYWORDS RTG.
 SOURCE Drosophila melanogaster
 ORGANISM Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Muscivora; Neoptera; Endopterygota; Diptera; Brachycera;
 1 (bases 1 to 85095)
 AUTHORS Celinker,S.E., Abayana,A., Arcina,T.T., Baxter,E., Blazel,R.G.,
 Butenoff,C., Champe,M., Chavez,C., Chew,M., Ciesiolka,L.,
 Doyle,C.W., Farfan,D.E., Galle,R., George,R.A., Harris,N.L.,
 Kestlin,K.A., Houston,K.A., Hummel,S.R., Kara,R., Kearney,L.,
 Kestlin,K.A., Kestlin,S.A., Li,Y., Lomtan,M.A., Madz,P.,
 Mosheiff,A.R., Mosheiff,B., Poon,W., Sequeira,B., Smith,H., Smith,
 S., Svitelsky,R.R., Van,K.H., Weinburg,T., Zhang,R., Zieran,L.L. and
 Rubin,G.M.
 TITLE Sequencing of Drosophila chromosome 2L, region 21C5-21D1
 JOURNAL unpublished (1998)
 REFERENCE 2 (bases 1 to 85095)
 AUTHORS Abmayor,S.E., George,R.A., Galle,R., Svitelsky,R.R., Hoskins,R.A.,
 Chew,M., Doyle,C.W., Farfan,D.E., Galle,R., George,R.A., Chavez,C.,
 Hummel,S.R., Kara,R., Kearney,L., Kestlin,K.A., Houston,K.A.,
 Lomtan,M.A., Madz,P., Mok,M.S., Mosheiff,A.R.,
 Mosheiff,M., Nixon,K., Pochle,J.M., Park,S., Pfeiffer,B., Punch,E.,
 Shit,E., Twomey,B., Van,K.H., Whiteley,K.R., Yee,A., Zhang,R.,

This sequence was generated from part of bacterial clone contigs on human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at

repeat_region


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NTID      94493924
VERSION   AL008970.2 GI:4493924
KEYWORDS  malaria parasite P. falciparum.
SOURCE    Plasmodium falciparum
ORGANISM  Eukaryota; Alveolates; Apicomplexa; Hemosporida; Plasmodium.
REFERENCE 1 (bases 1 to 11399)
AUTHORS   Hamlin, N., Bowman, S., Churcher, C., Lawson, D., Quail, M. and
          Barrett, B.
JOURNAL   Direct Submission
          Submitted (15-APR-1999) P. falciparum Genome Sequencing Consortium,
          Ch01, Sanger, Wellcome Trust Genome Campus, Hinxton, Cambridge
          On Mar 24, 1999 this sequence version replaced gi:3763998.
          For more information about this sequence see the Malaria Project,
          see http://www.sanger.ac.uk/Projects/P_falciparum. It may be that this
          sequence is not the entire insert of clone MAL3p4. It may be a
          shorter because we only sequence overlapping sections once, or
          longer because we arrange for a small overlap between neighbouring
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FEATURES             Location/Qualifiers
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 AUTHORS Chen, T., Bunting, M., Karin, F. D. and Thummel, C. S.
 TITLE Isolation and characterization of five Drosophila genes that encode related DNA binding domain proteins.
 JOURNAL Dev 8, 151, 176-191 (1992)
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 Db 313 GCTTACCACTGTCTCCATCCTCAACAG 338

RESULT 4
 AC007818.c DNA HTG 14-JUN-1999
 LOCUS AC007818.c
 DEFINITION Drosophila melanogaster chromosome 3 clone BACR02M05 (D785) RPCI-98
 02.4.3 map 188-988 strain y; cn bp, WORKING DRAFT SEQUENCE, 20
 kb contigs and pieces.

ACCESSION AC007818
 MID AC007818
 VERSION 95053146
 KEYWORDS AC007818.1 GI:5053146
 SOURCE HTG: PHASE1.
 ORGANISM *Drosophila melanogaster*
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 Muscivora; Muscidae; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 60056)
 GenBank, E. Abmayyan, A. Arcalini, T.T. Baxter, E. Blazek, R.G.,
 Buehner, C., Champe, M., Chavez, C., Cheu, M., Ciesiolka, L.,
 Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L.,
 Hoskins, R.A., Houston, K.A., Hummel, S.R., Katta, K., Kearney, L.,
 Kim, E., Lee, B., Lewis, S., Li, P., Lomoth, M.A., Mada, P.,
 Moshire, A.R., Moshire, N., Nixon, K., Pacלב, J.M., Park, S.,
 Pfeiffer, B., Poon, L., Sequeira, A., Sethi, H., Solari, E.,
 Svirskae, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieren, L.T. and
 Rubin, G.M.
 Direct Submission
 Submitted (14-JUN-1999) Drosophila genome center, Lawrence Berkeley
 Laboratory, MS 84-121, Berkeley, CA 94720, USA
 For further information about this sequence, including its location
 archive Web site (<http://www.fruitfly.org/sequence/>) or send email
 to bugreport@fruitfly.org. All contigs in this submission meet
 the following cutoffs: length >= 400 bases, phrap computed error
 rate <= 1/10.
 NOTE: This is a 'working draft' sequence. It currently
 consists of 20 contigs. The true order of the pieces
 is not known and their order in this sequence record is
 arbitrary. The gaps between contigs are of unknown
 size. This record will be updated with the finished sequence
 as soon as it is available and the accession number will
 be preserved.

1 893: contig of 893 bp in length
 894 973: gap of unknown length
 1964 1964: contig of 991 bp in length
 1965 2044: gap of unknown length
 1966 2044: gap of unknown length
 3653 3723: contig of 1608 bp in length
 3723 3723: contig of 1608 bp in length
 3723 5272: contig of 1540 bp in length
 5272 5272: contig of 1540 bp in length
 5353 6476: contig of 1124 bp in length
 6476 6476: contig of 1124 bp in length
 6557 6557: contig of 2113 bp in length
 6557 8749: gap of unknown length
 8749 8749: gap of unknown length
 8750 11281: contig of 2532 bp in length
 11281 11921: gap of unknown length
 11921 13355: contig of 1334 bp in length
 13355 13355: contig of 1334 bp in length
 13355 16234: contig of 2799 bp in length
 16234 16234: gap of unknown length
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 20047 20047: gap of unknown length
 20048 20127: gap of unknown length
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 20128 21987: contig of 1860 bp in length
 21987 21987: gap of unknown length
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 28787 32920: contig of 4054 bp in length
 32920 32920: gap of unknown length
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 35523 35523: gap of unknown length
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 41970 46511: contig of 4542 bp in length
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 /submitter="Lawrence Berkeley Laboratory, MS 84-121, Berkeley, CA 94720, USA"
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 Matches 192; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

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 Oy 1217 tccatcaggtgagtcacacag 1276
 Db 54017 GGCATCCGAGTACATCAAG 53958
 Oy 1277 ggcgcgctctgagagacacagagagagagagagagagagagagagagagagagagag 1336
 Db 53957 GCGACAGCTGTGGGTGGCGAG 53988
 Oy 1337 tccatcaggtgagtcacacag 1396
 Db 53987 TCCATCAGAGAGTACTACAG 53838

[illegible]

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Db	365	ttcaactgacgtgaccccccagacagatnaccacggctctggccatcagagaccctccg	424	
Oy	1310	gccatgaactacgaacgaacgtatgacgcgtccatccacgcgcgtattctacagaagagacatc	1369	
Db	425	gccatgaactacgaacgaacgtatgacgcgtccatccacgcgcgtattctacagaagagacatc	1369	
Oy	1370	cgaagacgaagacatctccacagcgtctctgtctcaattctgcagaccatctgagtgect	1429	
Db	485	cacagc---ctggccgcgcgacacgcgtacgtctcacaattgtgtgtgtgacccacagcccttc	541	
Oy	1430	gaccacgagctcgtaaacccgcgcctcacaaggcctcc	1465	
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AF000672				
LOCUS	AF000672	742 bp	mRNA	PRI
DEFINITION	Homo sapiens ELK variant mRNA, complete cds.			02-JAN-1999
ACCESSION	AF000672			
VERSION	AF000672.1	GI:1400455		
KEYWORDS				
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
AUTHORS	Eutheria; Primates; Cetartihmi; Homiidae; Homo.			
TITLE	Arxylc D.1 to 442			
NOTE	Novel family members HNEZ7, ELFR, and ELK among ERF-related genes			
JOURNAL	compressed with EMS-FLU1 in living tumor cell lines			
REFERENCE	2 (bases 1 to 742)			
AUTHORS	Arxylc D.N.T. and Kovar H.			
TITLE	Direct Submission			
JOURNAL	Annals (12 JAN 1997) Children's Cancer Research Institute, St.			
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	/db_xref="GI:4100456"			
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Best Local Similarity	64.6%;	Pred. No. 5;3e-06;		
Matches 159;	Conservative	0;	Mismatches 81;	Indels 6;
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Oy	1226	tgctctcaacgaaggaagagcttcaaacatttgagcttcgcccacgagtgccgcgcgc	1285	

[illegible]


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REFERENCE      3 (bases 1 to 1403)
AUTHORS       Delattre,O.
TITLE         Direct Submission
JOURNAL       Submitted (13-FEB-1997) O. Delattre, Institut Curie, Inserm U434,
              26 rue Duhm, Paris 75231 Cedex 05, Paris 75231 Cedex 05, FRANCE
COMMENT       On Feb 15, 1997, this sequence version replaced g1:1834485.
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ORIGIN
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Best Local Similarity 54.78; Pred. No. 6,9e-06;
Matches 214; Conservative 0; Mismatches 166; Indels 11; Gaps 2;

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DB 252 atccacctggaagcttctctcaagaagcttctctcaagaagcccccacagctatgacccgttc 311
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